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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                  Result
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2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
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9: sp_phage:*
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| 11155555555555555555555555555555555555   | 15.2<br>15.2<br>15.2<br>15.2<br>15.1<br>15.1  |
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## ALIGNMENTS

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000467;
01-JUL-1997
01-JUL-1997
01-DEC-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97258620; PubMed=9104814;
Lee S.Y., Lee S.Y., Choi Y.;
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61 ATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQS 120
                                                           RTIINKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERN 60
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Last sequence update)
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Pred. No. 1.1e-52;
; Mismatches 0;
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; BC000310; AAH00310.1; -.
InterPro; IRR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
Zinc-finger.
SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;
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9BWF2;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                    TRAF-INTERACTING PROTEIN
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217; Conserv
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0; Mismatches
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                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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01-JUL-1997
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Itawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.
Hayashizaki Y.
"Functional annotation of a full-length mouse cDNA collaboration of a full-length mo
SEQUENCE FROM N.A. MEDLINE=97258620; Pub Lee S.Y., Lee S.Y., C
                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTRIP.
TRAIP OR MTRIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 KTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERN 115
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                                                                                                      PubMed=9104814;
                                                           Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53149 MW;
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85.5%;
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Pred. No. 1.9e-44
9; Mismatches 1
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Matches
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Q922M8;
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Submitted (APR-2001) to t
EMBL; BC006929; AAH06929.
SEQUENCE 223 AA; 25584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE 4
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                                                                                                                  QRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK 206
                                                                                                                                                      QLPEVEEMIRDMGVGQSAVEQLAVYCVSLKK 151
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                                                                                                                                                                                                                                                         ATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQS 120
                                                                                                                                                                                                                                                                                                                                             ATVESTQNALNKAEMICSTLKKQMKFTEQRQDETKQAREEAHRIKCKMKTMEQIELLIQS
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134; Conserv
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25584 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Score 654; DB
8; Mismatches
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Pred. No. 1.9e
19; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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.6e-30;
les 9;
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.9e-44;
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Acanthomorpha; Acanthopterygii; Tel
Tetraodontidae; Takifuan
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                    Kobayashi C., Kobayashi S., Orii H., Agata K., Watanabe K. "Identification of two distinct muscles in the planarian, japonica, by the expression of myosin heavy chain genes."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; ABOL5484; BABA34954.1; -. HSSP; P24733; IWDC.
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FEBS Lett. 443:370-374(1999).
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC 1
EMBL; AJ010317; CAA09084.1; -.
Interpro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
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Paludicola; Dugesiidae; Dugesia.
NCBI_TaxID=6161;
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Dugesia japonica (Planarian).
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Mismatches 63
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PRINTS; PR00194; TROPOMYOSIN.
PRODOM; PD000355; MYOSIN_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSG; 1.
PROSITE; PS00125; CRYSTALLIN_BET PROSITE; PS00125; GLYSTALLIN_BET PROSITE; PS00126; GLYSTALLIN_BET PROSITE; PS00196; IQ; 1.
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InterPro; IPR004009; Myosin_N.
InterPro; IPR004009298; Myosin_tail.
InterPro; IPR0002938; Tropomyosin.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_N; 1.
  NON_TER
SEQUENCE
                                                                                                                     Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                              DNA Res. 6:197-205(1999).
EMBL; AB029004; BAA83033.1;
HSSP; P01100; 1FOS.
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                                                 InterPro;
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                                                    IPR002017; Spectrin
     529
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     AA;
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  61417
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22.7%;
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     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 178;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
     08D94249ACC63F22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529
                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
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ن.027;
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                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
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Query Match

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Best Local S
Matches 58
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                     Q9QZ84
Q9QZ84;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UIK7 PRELIMINARY;
Q9UIK7;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1998) to the EMBL; AB015617; BAA88763.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LEK1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoma."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakata T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                EASLLDLKEHASSLASSGLKKDSRLKTLEIALEQKKEECLKMESQLKKAHEAALEAR-AS
                                                                                                                                                                                                                                                                                                                                                                            EEMIRDMGVGQS-------AVEQLAVYCV----SLKKEYENLKEARKAS
                                                                                                                                                                                                                                                                                                                                                                                                                          LEEALAEKERTIERLK-----EQRDRDEREKQEEIDNYKKDLKDLKEKVSLLQGDLSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLLQSQLPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDMLDVKERKVNVLQK-----KIENLQEQLRDKEKQMSSLKERVKSLQADTTNTDTALTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEMSDRIQHLEREITRYKDESSKAQAEVDRLLEILKEVENEKNDKDKKTAEL-ESLTSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVADK - - - LRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEMIRDMGVGQS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15617; BAA88763.1; -. IPR002017; Spectrin. 948 AA; 108792 MW;
                        (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                    PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                           Created)
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
MYOSIN HEAVY CHAIN (FRAGMENT).
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                            J. Exp. Biol. 200:27-34(1997).
EMBL; D50475; BAA09068.l; -
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                            MEDLINE-97176447; PubMed-9023993; Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Wat "cDNA cloning of myosin heavy chain isoforms from muscle and their gene expression associated with tacclimation."; J. Exp. Biol. 200:27-34(1997). EMBL; D50475; BAA09068.1; -.
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"The cloning and analysis of LEK1 identifies
LEK/centromere protein F/mitosin gene family.
J. Biol. Chem. 27:18597-18604(1999).
EMBL; AF194970; AAF07196.1;
EMBL; MGI:1915046; 6530404A22Rik.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                           Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Cyprinus.
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MEDLINE=99303627; PubMed=10373470;
                           NON_TER
                                               PRINTS;
                                                                                                                                                                                                                                                                                        TISSUE-FAST MUSCLE;
MEDLINE-97176447; P
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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  AA;
                                               TROPOMYOSIN.
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ntifies variations
family.";
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Euteleostei;
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Best Local S
Matches 59
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa Chromosome 10 BAC OSJNBa0001014 genomic sequence.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC025783; AAK20041.1;
SEQUENCE 1578 AA; 178947 MW; CBB7ElDB68A821A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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EVHGYASHLEQELEQSKRKTMDFCKTLESLEAKLSSLQEDISLKEQSLLS
                                              ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMS
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8; Mismatches
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Pred. No. 0.081;
9; Mismatches 87,
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01-JAN-1998 (TrEMBLrel. 05, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotatic
MYOSIN HEAVY CHAIN.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Cypriniformes; Cyprinidae; Cyprinus.
NCBL_TaxID-7962;
  Q9EQN8;
Q9EQN8;
01-MAR-2001
01-MAR-2001
01-JUN-2001
MITOSIN (FRA
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042352;
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ProDom; PD000355; myosin_head;
SMART; SM00015; IQ: 1.
SMART; SM000242; MYSC; 1.
SEQUENCE 1931 AA; 221162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_k; 1.
Pfam; PF01576; Myosin_kail; 1.
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InterPro; IPR004009; myosin_N.
InterPro; IPR002928; myosin_tail.
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                                                                                                                                                                                                                                                                                                                                                                                                             1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000048; IQ.
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EMBL; D89991; BAA22068.1;
HSSP; P13538; 2MYS.
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MEDLINE=97352533; P
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59; Conser
      (FRAGMENT).
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(TrEMBLrel. I
                                                                                                                 PRELIMINARY;
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Pred. No. 0.14
9; Mismatches
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Euteleostei;
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Matches 54
                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-20062524; PubMed-10594536;

MEDLINE-20062524; PubMed-10594536;

Tsai L., Sun Y., Chao P., Ng H., Hung M.,

"Sequence analysis and expression of a cDI
allergen in Dermatophagoides farinae.";

""". Allergy 29:1606-1613(1999).
                 SEQUENCE FROM N.A. Tsai L.-C., Chao P.-L., Ng h
Tsai L.-C., Chao P.-L., to the
Submitted (FEB-2001) to the
EMBL; AF352244; AAK39511.1;
NON_TER 692 692
                                                                                                                                                                                                                                                                                                                                  MEDLINE-98389068; PubMed-9723675;
Tsai L.C., Chao P.L., Shen H.D., '
Hung M.W., Lee B.L., Chua K.Y.;
"Isolation and characterization o
farinae mite allergen.";
J. Allergy Clin. Immunol. 102:295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q967Z0;
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"Evolution of the internal repeat of mitosin.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ d
EMBL; AF182407; AAG43426.1; -.
InterPro; IPR000533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Dermatophagoides.
NCBI_TaxID-6954;
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01-DEC-2001 (TrEMBLrel. 19, Last se
01-DEC-2001 (TrEMBLrel. 19, Last an
PARAMYOSIN-LIKE ALLERGEN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
MCBI_TaxID-10090;
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692 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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37896
81372 MW;
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22.5%;
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                                                                                            H.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                      i.-P., Chua K.-Y.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 164.5;
Pred. No. 0.02
55; Mismatches
61FC6380C9D7C9E2 CRC64;
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                                                                                                                                                                                                                                           Hsieh K.,
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                                                                                                                                                                                                                                                                                                                                                                                          98-kd
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang T.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-97442456; PubMed-9295333;
MISUMI Y., Sohda M., Yano A., Fujiwara T., Ikehara Y.;
Molecular Characterization of GCP170, a 170-kDa Protein
With the Cytoplasmic Face of the Golgi Membrane.";
J. Biol. Chem. 272:23851-23858(1997).
EMBL; D63997; BAA33661.1; -.
EMBL; D63997; BAA33661.1; -.
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043241;
01-JUN-1998
01-JUN-1998
01-DEC-2001
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                                                                                               1252
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LTEQQG----RKELEGLQQLLQNVKSELEMAQEDLSMTQKDKFMLQAKVSELKNNMKTLLQ
                                                                                               AQFQAELAEARAQLQLLQKQL----DEQLSKQPVGNQEMENLKWEVDQKEREIQSLKQQLD
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                                                                                                                                                                                          KEQVAAAKVEAGHNRRHFKAASLELSEVKKELQAKEHLVQKLQAEADDLQIREGKHSQEI
                                                                                                                                                                                                                                          QQALGKAEMLCSTLKKQMKYLEQQQDETK------QAQEEAGRLRSKMKTME-
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60; Conservative
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                                                                                                                                        -LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARK
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 164; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
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Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                            Myosin.
SEQUENCE
                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                         Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00133; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Biol. 200:27-34(19 EMBL; D89990; BAA22067.1; EMBL; D50474; BAA09067.1; HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle and their gene acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90337;
01-NOV-1996
                                                                   1291
                                                                                                                                                           1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M.
"cDNA cloning of myosin heavy chain isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated myosin subfragment-1 isoforms from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=FAST
                                                                                                              1236
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004009;
InterPro; IPR002928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-FAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirayama Y., Watabe S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97352533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                  ProDom; PD000355;
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural differences in the crossbridge head
                                            157
                                                                                        112
  206
                                                                                                                                   60
                                                                                                                                                                                <u>,,</u>
 DKEIMSLKKKLTMLQ
                                                                                                                                                          EESTLQHEATAAALRKKQADSVAELGEQIDNLQRIKQKLEKEKSEYKMEIDDLSSNME--
                                                                                                                                                                                EENVLDREF - - -
                                            KEAR-----KASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSA
                                                                                        EQIELLLQSQLP-
                                                                                                              ----AVAKAKGNLEKMCRTLEDQLSEIKAKSDENSRQLNDMNAQRARLQTENGEFSRQL
                       | CEAKAELQRGMSKANSEVAQWRAKYETDAIQRTEELEESKKKLAQ
                                                                  EEKEALV-SQLTRGKQAFTQQIEDLKRHVEEEVKAKNALAHAVQSARHDCDLLREQYEEE
                                                                                                                                  NATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKT------M
                                                                                                                                                                                                                                                                                           SM00015; IQ; 1
SM00242; MYSC;
                                                                                                                                                                                                      Similarity
59; Conserv
                                                                                                                                                                                                                                                                                 PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                           IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000048;
                                                                                                                                                                                                                                                             1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738-1933 FROM N.A. SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                200:27-34(1997).
                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246:380-387(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ral MUSCLE;
PubMed=9208928;
                                                                                                                                                                                                                                                                                  IQ;
                                                                                                                                                                                                                                                                                                                 myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                   Myosin_tail
                                                                                                                                                                                                                                                                                                                                                                                              myosin_head Myosin_N.
                                                                                                                                                                                                               15.3%;
  220
                                                                                                                                                                                                                                                             221092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
08,
                                                                                                                                                                                                    50;
                                                                                                                                                                                                  Score 163; DB
Pred. No. 0.18
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                             LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEER
                                                                                       -EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL
                                                                                                                                                                                                                                                             CDF0CBAA475530F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kakinuma M., Watabe -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                                                                                  . 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
on update)
                                                                                                                                                                                                                           13;
                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carp fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
                                                                                                                                                                                                                          Length 1933;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                             CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ostariophysi;
                        RLQDAEESIEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skeletal
                                                                                                                                                                                                     60;
                                                                                                                                                                                                     Gaps
                        1406
                                                                                                              1290
                                                                                                                                                          1235
                                                                                                                                   111
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                                             205
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RESULT
OPPORT
OP
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Q9MIZ

ID Q9

AC Q9

DT Q9

DT Q1

DT Q1

DT Q1

RN Q9

RN Q0

R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
   Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99MI1;
Q99MI1;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLER. 19, Last annotation update)
RAB6-INTERACTING PROTEIN 2 ISOFORM B.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebratamammala; Eutheria; Rodentia; Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099MI2 PRELIMINARY; PRT; 976 AA. 099MI2; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence up 01-DEC-2001 (TrEMBLrel. 19, Last annotation RAB6-INTERACTING PROTEIN 2 ISOFORM A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/
EMBL; AF340028; AAK26381.1; -.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 976 AA; 111931 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rab6
                                                                                                                                                        Submitted (JAN-2001) to the EMBL; AF340029; AAK26382.1; InterPro; IPR002017; Spectr: SEQUENCE 1120 AA; 128330
                                                                                                                                                                                                                                                                                  Rab6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                           Monier S., Janoueix-Lerosey I., Jollivet 
"Characterization of a novel interaction
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Monier S., Janouei
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEMSDRIQQLEREISRYKDESSKAQTEVDRLLEILKEVENEKNDKDKKIAEL-ESLTSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEVADK----LRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASLLDIKEHASSLASSGLKKDSRLKTLEIALEQKKEECLKMESQLKKAHEATLEAR-AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEMIRDMGVGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEALADKERTIERLK-----EQRDRDEREKQEEIDTYKKDLKDLREKVSLLQGDLSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt KDMLDVKERKVNVLQK----KIENLQEQLRDKEKQMSSLKERVKSLQADTTNTDTALTT}
         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
58; Conserv
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Janoueix-Lerosey I., Jollivet ization of a novel interaction
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                        Spectrin.
128330 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%;
                               15.
24.
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                                   . 2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
   48;
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Pred. No. 0.11
48; Mismatches
Score 162; DE
Pred. No. 0.12
18; Mismatches
                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AVEQLAVYCV----SLKKEYENLKEARKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48731867C8D8CD6F
                                                                                                                                                        A542B526FAEDF9C7
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                        F., Goud
partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F., Goud
                               DB
.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
.11;
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                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                        Goud
   96;
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                                                               Length 1120;
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B
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                                                                                                                                                        CRC64
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                              small
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   38;
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                                                                                                                                                                                                                                                                                                              GTPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671
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   7;
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RESULT
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                                                                                                                                                                                 InterPro; IPR000048; I
InterPro; IPR001609; n
InterPro; IPR002928; N
InterPro; IPR000533; T
DNA-binding;
NON_TER
SEQUENCE 17
                                 ProDom; PD000355; myosin_head; 1.
smarT; SM00015; TQ; 1.
smarT; SM00242; MYSC; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.
PROSITE; PS50096; TQ; 1.
                                                                                                                       PRINTS;
                                                                                                                                            Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head;
Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                             Kobayashi C., Kobayashi S., Orii H., Agata K., Watanabe K., "Identification of two distinct muscles in the planarian, I japonica, by the expression of myosin heavy chain genes."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTION REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
NCBI_TaxID=6161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096063
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Kobatashi C., Agat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, La
01-DEC-2001 (TrEMBLrel. 19, La
MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                             InterPro; IPR001064;
InterPro; IPR001637;
InterPro; IPR000524;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Kobatashi
Submitted
                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                      HSSP; P08799;
                                                                                                                                                                                                                                                                                 EMBL; AB015485; BAA34955.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEVADK----LRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDMLDVKERKVNVLQK-----KIENLQEQLRDKEKQMSSLKERVKSLQADTTNTDTALTT
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                                                                                                           PR00035; HTHGNTR.
PR00193; MYOSINHE
PR00194; TROPOMYC
                                                                                                                                                                                                                                                                                                                                                                                           C., Agata K.,
(JUN-1998) to
 1743
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                        Transcription regulation
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                                                                                             TROPOMYOSIN.; myosin_head;
                                                                                                                       MYOSINHEAVY
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GlnA_adenyltn.
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Myosin_tail
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 200417
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Last annotation update)
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0D4A821FA6CFF7C2
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TRANSCRIPTIONAL
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 CRC64
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Query Match
Best Local Similarity
Matches 51; Conserv

Conservative

58;

Score 162; DB Pred. No. 0.19; 8; Mismatches

5; 95;

Length 1743; Indels

36;

Gaps

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Best Loc
Matches
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EMBL; AB039672; BAB12571.1; -.

HSSP; P13538; 2MYS.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostel; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Sciaenidae; Pennahia.
                             1278
                                                                                                                                    1168
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                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-FAST MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennahia argentata.
                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                          PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                         Piam;
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=118565;
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                                                                                                                                                             KLFFDLAQEEENVLDREF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQ
YCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQT----VYSELDQAKLELKSAQK 200
                         ENGEFTRQVEEKEALVSQLTRGKQAFTQQIEELKR----QIEEEVKAKNALAHGVQSARH
                                                   ----TKQAQEEAGRL----RSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAV
                                                                              DLSSNME-----AVAKAKGNLEKMCRTLEDQLSELKTKNDENVRQINDMSGQRARLLT 1277
                                                                                                        TLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDE--------
                                                                                                                                   KLRRDL---EESTLQHEATAAALRKKQADSVAELGEQIDNLQRVKQKLEKEKSEYKMEID 1224
                                                                                                                                                                                                                                                                                                                                   PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
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                                                                                                                                                                                                                                                                                                                                                                            PF00612; IQ;
                                                                                                                                                                                                                                                                    SM00242; MYSc;
E; PS50096; IQ;
                                                                                                                                                                                         63;
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                                                                                                                                                                                                                                                         1930
                                                                                                                                                                                        Conservative
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24.2%;
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                                                                                                                                                                                     Score 162; DE
Pred. No. 0.21
19; Mismatches
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                                                                                                                                                                                        86;
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01-OCT-2001
01-OCT-2001
MEA2/GOLGA3
MEA2/GOLGA3.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1392 -LQDAEEQIEAVNSKCASLE 1410
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Submitted (JUL-1999)
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                          KL-TMLQ
                                                                                                                                KQAQEEAGRIRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE 154
                                                                                                                                                                      KEQMAAARIEAGHNRRHFKAATLELSEVKKELQAKEHLVQTLQAEVDELQIQDGKHSQEI 1207
                                                                                                                                                                                                                                                          QEEENVLDREFLKNELD-----NVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSL
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                                                                                  NLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK 214
                                                                                                              AQFQTELAEARTQLQ-
                                                                                                                                                                                                  QQALGKA-----
                                                    SLKQQLDLTEQQG---
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AB029535;
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57; Conservative
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1 (TrEMBLrel.
3 PROTEIN.
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                          220
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Q1-JUN-2001
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Q9QYT3;
Q1-MAY-2000
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EMBL; AB029537; BAA8
EMBL; AB029521; BAA8
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Matsukuma S.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY
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Mouse.":
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                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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JOINED.
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Pred. No. 0.18
48; Mismatches
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Sciurognathi; Muridae
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; Murinae; Mus
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and heterologous expression.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ daventer of the EMBL/GenBank/DDBJ daventer of the theory in 18002928; Myosin_tail.
InterPro: IPR001854; Ribosomal_L29.
Pfam; PF01576; Myosin_tail; 1.
SEQUENCE 876 AA; 102454 MW; C99475EE7A0DAE52
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
InterPro; IPR002928; myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF001576; Myosin_tail; 1.
                                                                                                         alternative splicing from the myo
J. Mol. Biol. 295:169-178(2000).
EMBL; AF183909; AAF62391.1; -.
HSSP; P24733; 1WDC.
                                                                                                                                                                                                                                       Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
Pectinoidea; Pectinidae; Argopecten.
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Acariformes; Sarcoptiformes; Astigmata; Sarcoptoidea; Sarcopti
                                                                                                                                                                     Yamada A.,
                                                                                                                                                                                     MEDLINE=20090924; PubMed=10623517;
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AA; 102454 MW; C99475EE7A0DAE52 CRC64;
                                                                                                                                              protein in molluscan catc
ing from the myosin heavy
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MUSCLE SPECIFIC ISOFORM
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Pred. No. 0.12;
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Q61043;
01-NOV-1996
01-NOV-1996
01-DEC-2001
NINEIN.
                                                                                                                                                                                              InterPro; SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ;
                     1698
                                                                                                     1592
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J. Cell Sci. 108:0-0(1996).

EMBL; U40342; AAA83234.1; -.

MGD; MGI:105108; Nin.
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                              1638
                                                                                                                                                                                                                                                           "Molecular characterisation
                                                                                                                                                                                                                                                                     Bouckson-Castaing V., Belkaid Y., Milon G.,
                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                   QTMVEKL-----KKQVSDLKIKNQQLDSENIELSQKNSQNKEE-----LKTLNQRL 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKLEKDKKDLKREMDDLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLKSTQENVEDLERVKRELEENVRRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEE
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                                                                               ATVVSLQQALG-----KAEMLCSTLKKQMKYLEQQQDETKQAQE-EAGRLRSKMKTMEQI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY 185
                     NLLLKDELERLKQLHRCPDLSDLQQKMSSVLSYNEKLLKEKEVLSEELKSCADKLAESSL
                                        ELLLQSQLPEVEEMIR - - DMGVGQSAVEQLAVYCVSLKKEYENLKEARKASG - - -
                                                             AEMLCQREEPGACTSEKWEQENASLKEELDHYKVQTSTLVSSLEAELSRIKLQTHVMEQE
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58; Conserv
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2168 AA;
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249168 MW;
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28.1%;
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Crocker P.R.;
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Last sequence update)
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                                                                                                                                                                                                                                                            of ninein,
                                                                                                                                           Score 160.5;
Pred. No. 0.28
4; Mismatches
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Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                  Murinae;
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RESULT
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AC Q9

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Best Local
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01-DEC-2001
                                                                                                                                                                                                                                                                                                  Q9NJ22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A. Champe M., Chavez C., Dorsett V., Frafan D., Fri Gonzalez M., Guarin H., Li P., Liao G., Miranda Nunco J., Pacleb J., Paragas V., Park S., Phouan Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ da EMBL; AY060610; AALI28158.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Y, CN BW SP;
Stapleton M., Brokstein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95SS5
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                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN CATCH (SMOOTH) MUSCLE SPECIFIC
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  SEQUENCE FROM N.A. MEDLINE-20090924;
                                                                   Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
NCBI_TaxID=31199;
                                                                                                                                                                   MHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLQTVYSELD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
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    PubMed=10623517;
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Last sequence update)
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Best Local S
Matches 57
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InterPro; IPR001609; myosin_head.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR00292017; Spectrin.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00063; Myosin_tail; 1.
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Q9NJ21;
01-OCT-2000
                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-20090924; PubMed-10623517;
Yamada A., Yoshio M., Oiwa K., Nyitray L.;
"Catchin, a novel protein in molluscan catc
"Catchin, a novel protein the myosin heavy
J. MO1. Biol. 295:169-178(2000).

EMBL; AF183009; AAF62394.1; -.
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
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    ProDom;
                        PRINTS;
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01-DEC-2001
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n catch muscles, I
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Matches 57
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Best Local S
Matches 57
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PFNNTS; PR00194; TROPOMYOSIN.
ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
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PROSITE; PS50096;
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SEQUENCE 1243 AA
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HSSP; P24733; IWDC.
InterPro; IPR000048; IQ.
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"Catchin, a novel protein in molluscan catternative splicing from the myosin heavy
J. Mol. Biol. 295:169-178(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Moilusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
NCBI_TaxID=31199;
                                                                                                                                                                                                                                    SEQUENCE
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57; Conserv
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Pred. No. 0.19;
9; Mismatches
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Pred.
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Best Local 9
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Pfam; PF00612; IQ; 2.
Pfam; PF00063; Myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00193; MYOSINHEAVY.
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Q17042;
Q1-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nyitray L., Janeso A., Ochiai Y., Graf L., Szent-Gyorgyi A.G.; "Scallop striated and smooth muscle myosin heavy-chain isoforms produced by alternative RNA splicing from a single gene."; proc. Natl. Acad. Sci. U.S.A. 91:12686-12690(1994).
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NCBI_TaxID=31199;
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Eukaryota; Metazoa; Mollusca; Bivalvia;
 1215
                                                  1172
                                                                                                                                                      1058
                                                                                                                                                                                                                                                                                                                    ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=MUSCLE, CAI
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SMART; SM00242; MYSC;
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InterPro; IPR002928; Myosin_tail.
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Interpro; IPR001609; myosin_head.
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                          186
                                                                           126
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                                                                                                                   LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV 125
                                                                                                                                                   DLKSTQENVEDLERVKRELEENVRRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEE
                                                                                                                                                                             DLAQEEENVLDREFLKNEL-DNVR---AQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS 65
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SKSEKEKQQLRSEVEDLQAQIQHISKNK 1242
                         SELDQAKLELKSAQKDLQSADKEIMSLK 213
                                                 LKIRRDL - - - EEASLQHEAQISALRKKHQD - - -
                                                                         EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY 185
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                                                                                                                                                                                                                                                                    1951 AA;
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Pred. No. 0.29;
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annotation
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on update)
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Best Local
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                                                                                                                                                                                                            Q07380
Q07380;
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  Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomy
Saccharomycetales; Saccharomycetaceae; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1318
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Pfam; PF00063; myOsin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myOsin_head; 1.
SMART; SM00242; MYSC; 1.
SEQUENCE 2139 AA; 245225 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ EMBL; L03534; AAB48065.1; -. HSSP; P08799; IMND.
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                                                                                  USO1 OR YDL058W.
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                                                                                                                                                                                                                                                                                                                                                                                                                   DKEIMSLKKK
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                                                                                                                                                                                                                                    PRELIMINARY;
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24.0%;
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Last sequence update)
Last annotation update)
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Pred. No. 0.32;
                               Saccharomycotina;
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     Saccharomyces
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                             Saccharomycetes;
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Best Local S
Matches 61
                                             Pfam; PF00612; IQ; 2.
Pfam; PF00663; myosin_head; 1.
Pfam; PF02736; myosin_m; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; mYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                Q9TV61; PRELIMINARY;
Q9TV61; O1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bloecker H., Brandt P.;
submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; Z74106; CAA98621.1; -.
EMBL; Z74105; CAA98620.1; -.
SGD; S0002216; USO1.
InterPro; IPR002017; Spectrin.
SEQUENCE 1790 AA; 206450 MW; 90062544F55A5
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-LANDRACE; TISSUE-SKELETAL MUSCLE;
STRAIN-LANDRACE; TISSUE-SKELETAL MUSCLE;
Chikuni K., Tanabe R., Muroya S., Nakajima
"Differences in molecular structure among t
chain-2a, -2x, and -2b isoforms.";
Meat Sci. 57:311-317(2001).
Meat Sci. 57:311-317(2001).
                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                        SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1596
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                                                                                                                       InterPro; IPR001609; myosin_head.
InterPro; IPR004009; myosin_N.
InterPro; IPR002928; myosin_tail.
                                                                                                                                                              InterPro; IPR000048; IQ.
                                                                                                                                                                             HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                           MYOSIN HEAVY CHAIN 2X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDLQSADKEIMSLKKKL
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              PS50096; IQ;
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Last sequence update)
Last annotation update)
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Pred. No. 0.29
57; Mismatches
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  B702ADB599602ECB CRC64;
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                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 56
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Best Local S
Matches 55
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Q26079;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-DEC-2001 (TrEMBLrel. 19, L
MYOSIN HEAVY CHAIN.
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_k; 1.
Pfam; PF01576; Myosin_tail; 1.
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InterPro;
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                                              1113
                                                                                                                                            1053
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ProDom; PD000355; myosin_head;
SMART; SM00015; IG; 1.
SMART; SM00242; MYSC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Placopecten magellanicus (Sea scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
Pectinoidea; Pectinidae; Placopecten.
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  121
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                                                                                                                                                                                                                                                           Local Similarity
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QLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSK 180
                                                                          ATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQS
                                              ARIEELEEELEAERNARSKVEKQRAELNRELEELGERLDEAGG-----ATSAQIELNKKR 1167
                                                                                                                                          SKVEQDLKSTQENVEDLERVKRELEENVRRKEAEITTLNSKLEDEQNLVSQLQRKIKELQ 1112
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                                                                                                                                                                                                                                       56;
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                                                                                                                                                                                                                                                                                                                                                                                  PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001609; myosin_head.
IPR004009; Myosin_N.
IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                           1941
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                               IQ;
                                                                                                                                                                                                                                                           14.9%;
27.5%;
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24.28;
                                                                                                                                                                                                                                                                                                                                                           223243
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                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence u
                                                                                                                                                                                                                                                         Score 158.5; D
Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                           E2AD1637FFDB8127
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10 0.
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.31;
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                                                                                                                                                                                                                                     72;
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                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                            Length 1941;
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binding
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Best Local Similarity
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SKELETAL MYOSIN HEAVY CHAIN (FRAGMENT).
Thunnus thynnus (Bluefin tuna),
Eukaryota; Metazoa; Chordata; Caraniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
                                                                                     Q22276 PRELIMINARY;
Q22276, Q22294;
Q12276, Q22294;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91520;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91520
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                    Caenorhabditis elegans
                                            T07C4.10 PROTEIN.
    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                           LKKEYENLKEAR------KASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGEFSRQIEEKDALVSQLTRGKQAYTQQIEELKRHIEEEIKAKNALAHAVQSARHDCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----MEQIEL--LLQSQLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSSNME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLRRDL---EESTLQHEATSASLRKKQADSVAELGEQIDNLQRVKQKLEKEKSEYKMEID
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                                                                                                                                                                                                                                                                                           AEESIEAVNSKCASLEKTKORLO
                                                                                                                                                                                                                                                                                                                                                                                   LREQYEEEQEAKGELQRGMSKANSEVAQWRTKYETDAIQRTEELLEEAKKKLAQ----RLQD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
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    Nematoda;
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24.08;
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                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                      Created)
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Pred. No. 0.18;
8; Mismatches
                                                                                                                                                                                                                                                                                             272
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  Chromadorea;
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                                                                                                                                                                                PRT;
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  Rhabditida; Rhabditoidea;
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                                                                                        update)
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SO DE RESERVATOR DE LA COMPTANTA DE LA COMPTAN
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Best Local
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Submitted (NOV-1996) to the EMBL/Ge
EMBL; Z48055; CAA88136.1; -
EMBL; Z29443; CAA88136.1; JOINED.
EMBL; Z29443; CAA82580.1; -
EMBL; Z29443; CAA82580.1; JOINED.
EMBL; Z19443; CAA82580.1; JOINED.
EMBL; Z19443; CAA82580.1; JOINED.
EMBL; Z184055; CAA82580.1; JOINED.
SEQUENCE 1138 AA; 132785 MW; DF
                                                                                       InterPro; IPR002928; Myosin_tail
InterPro; IPR002017; Spectrin.
Pfam; PP00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF02736; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00133; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                           Janes D.P., Patel H., Chantler P.D.;
"Primary structure of myosin from the striated adductor atlantic scallop, Pecten maximus.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF134172; AAD52842.1; ...
HSSP; P24733; IWDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pecten maximus (King scallop) (Pilgrim's clam).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9U7E3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9U7E3;
                                               SMART;
                                                                                                                                                                                                                                                                                                   InterPro; IPR001609; myosin_head.
InterPro; IPR004009; myosin_n.
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=ADDUCTOR MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pectinoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSQVIIDTLRDTLEERNATVVSLQQALGKAEML--CSTLKKQMKYLEQQQDETKQAQEEA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTIINKLFFDLAQEEENVLDREF-LKNELDNVRAQL---------
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                                             SM00015; IQ; 1
SM00242; MYSC;
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                          PS50096;
1940
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ĀΑ;
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Spectrin.
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24.78;
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Last sequence update)
Last annotation updat
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CRC64;
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Query Match

14.78;

Score

156.5;

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Length 1940;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUS-EYE, AND RETINA;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC016069; AAH16069.1;
SEQUENCE 959 AA; 106983 MW; 2C05DC35E899DB1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O91WE7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO TRANSCYTOSIS ASSOCIATED PROTEIN.
                  P92021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                              71 GKAEMLCSTLKKQMKYLEQQQDE----TKQAQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                 TOSKKEQDDLLVLLADQDQKILSLKSKL
                                                                                               KSAQKD------LQSADKEIMSLKKKL 216
                                                                                                                                   AAKTTDVEGRLSALLQETKELKNEIKALSEERTAIQKQLDSSNSTIAILQTEKDKLDLEV
                                                                                                                                                                                    PPRDPEQVAELKQELTALKSQLCSQSLEITRLQTENCELLQRAETLAKSVPVEGESEHVS
                                                                                                                                                                                                                                                                                                                                                                    EENVLDREFLK -- NELDNV -- RAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQAL 70
                                                                                                                                                                                                                                      DGAQVNGIQPEEISRLREEIEELKSQQALLQGQLAEKDSLIENLKSSQASGMSEQASATC
                                                                                                                                                                                                                                                                                       REQDIQLEELKQQVSTLKCQNEQIQTAVTQQASQIQQHKDQYNLLKVQLGKDNHHQGSHG
                                                                                                                                                                                                                                                                                                                                          EYMIFDHEFTKLVKELEGVITKAIYKSSEEDKKEEEV----KKTLEQHDNIVTHYKNMI 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLLQSQLPEV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLAQEEENVLDREFLKNEL-DNVR---AQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS
                                                                                                                                                                                                                                                              ------EEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSA--VEQLAVYC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLEKDKKDIKREMDDLES 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELDQAKLELKSAQKDLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKIRRDL---EEASLOHEAQISALRKKHOD-----AANEMADQV------DQLQKVK 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEELEAERNARAKVEKQRAELNRELEELGERLDEAGG-----ATSAQIELNKKRE-AEL
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity 19.5
64; Conservative
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                      VSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLEL
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                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                            Score 155.5; D
Pred. No. 0.25;
2; Mismatches
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Sciurognathi; Muridae;
                  PRT;
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01-MAY 1997 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
T10G3.5 PROTEIN.
                                                                                                                                                                                                                                                      Interpro; IPRO00306; Znf_FYVE.

Pfam; PF01363; FYVE; 1.

SMART; SM00064; FYVE; 1.

SMART; SM00035; ZnF_C2H2; 1.

PROSITE; PS00028; EF_HAND; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

SEQUENCE 1164 AA; 135041 MW; 0C8C438680E755C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81118; CAB03330.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                    none;
                                                 818
                                                                         124
                         184
                                                                                                                                              700
                                                                                               760
                                                                                                               64 VSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLP 123
                                                                                                                                                                    22 EFLKNELDNVRAQLSQKDK-----EKRDSQVIIDTLRDTL------
                                                                                                                                            EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQT
                        VYSELDQAKLELKSAQKDLQSADKEIMSLK 213
                                                TTQE--RDELTATS--ESLRTECENLNSKIQSIEESRRHAEEKGSENLERMITEKSRLE-
                                                                                               KSVQEQLMKEKETSGEEKNQLISVKSQLEELKTEVERL--IRSEEEKTQEIEKLKSAVTA
--KDIEERESTIQSIQEALETKDNEIESLK
                                                                                                                                                                                             Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                             IPR002048; EF-hand.
IPR000822; Znf-C2H2
IPR000306; Znf_FYVE
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                         51; Mismatches
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                       Score 155.5;
Pred. No. 0.
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Search completed: September 4, 2002, 16:16:02 Job time: 1486 sec

